EXHIBIT A

01/11/06 WED 17:48 FAX 512 536 4598   FULBRIGHT & JAWORSKI   ☑010

lalign output for X62480 vs. ID NO:8   Page 1 of 3

lalign output for X62480 vs. ID NO:8

[ISREC-Server] Date: Thu Jan 5 0:49:32 Europe/Zurich 2006

LALIGN finds the best local alignments between two sequences version 2.0u66 September 1998 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381 resetting to DNA matrix

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Comparison of:
(A) ./wwwtmp/lalign/.22838.1.seq X62480
(B) ./wwwtmp/lalign/.22838.2.seq ID NO:8
using matrix file: DNA, gap penalties: -14/-4

  76.0% identity in 770 nt overlap; score: 1865 E(10,000): 1.2e-146

            540       550       560       570       580
X62480 TCTTGCGGTGTCTTGGCAACATTCTTGTTGGAAG-ATACCAGA--AGGTTGCTC---CAC
       :::: : :   :  ::::::    :::::::::::::: ::: :::   :::::::::    :::
ID     TCTTTCAGAATTGTGGCA---TTCTTGTTGGAAGCATAGCAGTGTAGGTTGCTCATTCAC
           150       160       170       180       190

            590       600       610       620       630       640
X62480 GGGTAATCTTGACACGTATGTAAAGTGATGAGGAACATTGAACGAACATTGGCATGTA-A
       :: ::::::: :::::::      :::::::::::::::: :   ::::::  ::::::::::::::: :
ID     GGATAATCTCGACACGT----AAAGTGATGAGGAATACGGAACGACCATTGGCATGTAGA
          200       210       220       230       240       250

            650       660       670       680       690       700
X62480 GCTCTAT-AATTGGTGTTATCCATA--ACAACGTCGCAGAACATCACAAA-TTGCACGTC
       ::: :::  :::::::::::::::::::       :::::::::::::::::::::: ::::::::::::
ID     GCTGTATGAATTGGTGTTATCCATACAACAAC-TCGCAGAACATCACAAAATTGCACGTC
          260       270       280       290       300      ,310

            710       720       730       740       750
X62480 AAGGGATTGGGTCAGAAACAAATCGTCTCCGTGTA-------CAACGAAGTG---GTGAG
       :: :::::::::::::::::::::::::::::::::: ::::       ::: ::::::   :::::
ID     AATGGATTGGGTCAGAAACAAATCGTCTCCTTGTAGCTTGTACAATGAAGTGATGGTGAG
          320       330       340       350       360       370

            760       770       780       790
X62480 TCATGAGCCA---TGTT--GATCTGATATATAC-----ATAGCACACACGACATCA---C
       :::::::: ::    :: :  ::::::::::::::::       :::::: :::::::::::: ::     :
ID     TCATGAGTCACACTGATCCGATCTGATATATATGCCAAATAGCTCACACGACAACATTAC
          380       390       400       410       420       430

        800       810       820       830       840       850
X62480 AAACAAGTC-ATACTA--CATTACAGAGTTAGTTTCACCTTTCAAGTAAAAACAAAGTAG
       :::::::  :  :::::::   ::: :::  ::::  ::::::     :  ::    ::  ::   :::::
ID     AAACAACCCCATACTATACATCACAAAGTTTGTTTCA----TGAAAAAACAAATAAGTAT
          440       450       460       470       480       490

        860    :  870       880       890       900       910
X62480 GCCGGAGAGAGGACAATAATCCTTG----ACGTGTAAAGTGAATTTACAAAGCCATATAT
       ::  ::::: :   :::::::::::::::::       :::  ::::::::::::::::::::::::::::::::::
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ID        GCAGGAGGG--GACAATAATCCTTGCTTGACGCGTAAAGTGAATTTACAAAGCCATATAT
             500       510       520       530       540

          920            930       940       950
X62480 CAATTTATATCTAATT--------CGTTTCATGTA-----GAT----ATCAACAACC---
       ::: :::::::::::          :::: :: ::     :::  :::::::::::
ID     CAACCTATATCTAATTAATAAGTTCGTTATATATACGCACGATGATCATCAACAACCGTA
       550       560       570       580       590       600

          960       970       980       990      1000
X62480 --TGTAAAAGGCAACAAATTGAGCCACGCAAAATTACA-AGTGAGTCCAAATAA------
         ::: ::::::::::::: :::::::::::::::: : :: : ::: :::: :: :
ID     CCTGTGAAAGGCAACAAAATGAGCCACGCAAAAATGCAGAATGAATCCATATGATGACGA
       610       620       630       640       650       660

          1010      1020      1030      1040      1050
X62480 ----ACCCTCA-CATGCTACATAAAAGTGAATGATGAGTCATGTATATCTGGCAAGAAAC
          :: :::   : :::::::::::: :::::::::::::::::: :::: :::::::::::::
ID     ACGTACACTCGGCTTGCTACATAAA-GTGAATGATGAGTCATAAATATTTGGCAAGAAAC
       670       680       690      .700       710       720

          1060      1070          1080   ·  1090      1100      1110
X62480 TGTAGAAGCTACA------GTCATCGGTAGCAAAGAAACACAAGAAAATGTGCTAATAAAA
         ::  :::::::::       ::: :: :::::: :: :::::::::::: :::::::::: ::
ID     CGTGAAAGCTACACAGCCGTCGTCAGTAGCACAGGAACACAAGAAACTGTGCTAATCGAA
       730       740       750       760       770       780

          1120      1130      1140      1150      1160      1170
X62480 GCTATAAATAACCCTCGTACGCCTATGCACATCTCCATCACCACCACTGGTCTTCATTCA
       ::::::::::::::::: ::: ::::::::::: ::::::::::::::: ::   : :  ::::
ID     GCTATAAATAACCCTAGTATGCCTATGCACTTCTCCATCACCACTACCCATAT--CTTCA
       790       800       810       820       830       840

          1180      1190      1200      1210      1220
X62480 GCCTATTAACTTATATCTATCTACTCCAGAGCAGACAAGAACTCGACACC
       : :::::  :: : :  ::::::::::::::   :::   : :::::::::
ID     GTCTATTTACCT-TCTCTATCTACTCCAGAGAGCACAGAAGATCGACACC
       850       860       870       880       890
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    56.9% identity in 253 nt overlap; score:  134 E(10,000):  0.026
          900       910       920       930       940       950
X62480 TTACAAAG--CCATATATCAATTTATATCTAA-TTCGTTTCATGTAGATATCAACAACC-
       :::::::    ::  ::: : ::  ::  : :: ::  :::::::: : : :   :: ::
ID     TTACAAACAACCCCATA-CTATACATCACAAAGTTTGTTTCATGAAAAAACAAATAAGTA
          440       450       460       470       480

          960       970       980       990      1000
X62480 TGTAAAAGGCAACAAATTGAGCCACGCAAAAT---TACAAGTGAGTCCAAATAAACCCTC
       :: :  ::: ::::  : : ::  ::  :       :: :::::: :  : :  :: ::
ID     TGCAGGAGGGGACAA--TAATCCTTGCTTGACGCGTA-AAGTGAATTTACA--AAGCCAT
       490       500       510       520       530       540

          1010      1020      1030      1040      1050      1060
X62480 ACATGCTACATAAAAGTGAATGATGAGTCATGTATATCTG-GCAAGA--AAC-TGTAGAA
       : :: : :: :    : : :: ::  :::::       ::::: ::  :  : :  : :: ::
ID     ATAT-CAACCTATATCTAATTAATAAGTTCGTTATATATACGCACGATGATCATCAACAA
          550       560       570       580       590       600
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·. ·01/11/06 WED 17:49 FAX 512 536 4598   FULBRIGHT & JAWORSKI   ☑012

ᴬⁱᵍⁱᵗ Output for X62480 vs. ID NO:8

Page 3 of 3

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           1070       1080       1090       1100       1110 ·     1120
X62480  GC-TACA-GTCATCGGTAGCAAAGAAACACAAGAAAATGTGCTAATAAAAGCTATAA-AT
        : :::   :: :   :: : :::::    :  :: : :::   :::  :   :: : :::  ::
ID      CCGTACCTGTGAAAGGCAACAAAATGAGCCACGCAAAAATGCAGAATGAATCCATATGAT
           610        620        630        640        650        660


           1130
X62480  AACCCTCGTACGC
         ::    ::::: :
ID      GACGAACGTACAC
           670
```

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        58.9% identity in 190 nt overlap; score:   118 E(10,000):    0.57

           880        890          ·  900          910        920
X62480  ATAATCCTTGACGTGTAAAGTGA------ATTTACAAAG-CCAT----ATATCAATTTAT
        ::::::  : ::: ::::::::::     ::    :: : ::::   :: :   :  : :
ID      ATAATC-TCGACACGTAAAGTGATGAGGAATACGGAACGACCATTGGCATGTAGAGCTGT
           210        220        230        240        250        260

           930        940        950        960        970
X62480  ATCTAATTCGTTTCATGTAGATATCAACAACCTGTAAAAGGCAACAAA-TTGAGCCACGC
        ::   :::: :: : ::  : :   ::::::: : : ::    :::::: :::    ::::
ID      ATG-AATTGGTGTTATCCATA---CAACAACTCGCAGAACATCACAAAATTG---CACGT
           270        280        290        300        310

           980        990       1000       1010       1020       1030
X62480  AAAATTACAAGTGAGTCC-AAATAAACCCTCACAT----GCT---ACATAAAAGTGAATG
        ::   :    :: :!:  ::: ::: ::: :     ::: :::    ::::::: ::
ID      CAATGGAT---TGGGTCAGAAACAAATCGTCTCCTTGTAGCTTGTACAATGAAGTGA-TG
           320        330        340        350        360

           1040
X62480  ATGAGTCATG
        ::::::::::
ID      GTGAGTCATG
           370
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Back to ISREC bioinformatics group home page

http://www.ch.embnet.org/cgi-bin/LALIGN form parser

PAGE 12/12 * RCVD AT 1/11/2006 6:46:00 PM [Eastern Standard Time] * SVR:USPTO-EFXRF-6/27 * DNIS:2738300 * CSID:512 536 4598 * DURATION (mm-ss):03-24   2006